

#2 1/22



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RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/09/901,106

TIME: 11:05:42

Input Set : N:\Crf3\RULE60\09901106.raw

Output Set: N:\CRF3\02072002\I901106.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Garoff, Henrik

6 Liljestrom, Peter

8 (ii) TITLE OF INVENTION: DNA Expression Systems Based on
9 Alphaviruses

11 (iii) NUMBER OF SEQUENCES: 27

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Birch, Stewart, Kolasch & Birch

15 (B) STREET: P.O. Box 747

16 (C) CITY: Falls Church

17 (D) STATE: Virginia

18 (E) COUNTRY: USA

19 (F) ZIP: 22040-0747

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/901,106

C--> 29 (B) FILING DATE: 10-Jul-2001

30 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/07/920,281C

35 (B) FILING DATE: 13-AUG-1992

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Murphy Jr., Gerald M.

40 (B) REGISTRATION NUMBER: 28,977

41 (C) REFERENCE/DOCKET NUMBER: 828-103P

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 703-241-1300

45 (B) TELEFAX: 703-241-2848

46 (C) TELEX: 248345

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 11517 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: RNA (genomic)

59 (iii) HYPOTHETICAL: NO

61 (iv) ANTI-SENSE: NO

ENTERED

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63      (vi) ORIGINAL SOURCE:
64          (A) ORGANISM: Semliki Forest Virus
66      (ix) FEATURE:
67          (A) NAME/KEY: -
68          (B) LOCATION: 1..11517
69          (D) OTHER INFORMATION: /label= genome
70 /note= "Semliki Forest Virus complete nucleotide
71 sequence, presented as a cloned DNA sequence; see
72 Figure 5."
74      (ix) FEATURE:
75          (A) NAME/KEY: CDS
76          (B) LOCATION: 87..7379
77          (D) OTHER INFORMATION: /product= "SFV polyprotein"
79      (ix) FEATURE:
80          (A) NAME/KEY: CDS
81          (B) LOCATION: 7421..11179
82          (D) OTHER INFORMATION: /product= "SFV polyprotein"
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
87 GATGGCGGAT GTGTGACATA CACGACGCCA AAAGATTTTG TTCCAGCTCC TGCCACCTCC      60
89 GCTACGCGAG AGATTAACCA CCCACG ATG GCC GCC AAA GTG CAT GTT GAT ATT      113
90          Met Ala Ala Lys Val His Val Asp Ile
91          1          5
93 GAG GCT GAC AGC CCA TTC ATC AAG TCT TTG CAG AAG GCA TTT CCG TCG      161
94 Glu Ala Asp Ser Pro Phe Ile Lys Ser Leu Gln Lys Ala Phe Pro Ser
95 10          15          20          25
97 TTC GAG GTG GAG TCA TTG CAG GTC ACA CCA AAT GAC CAT GCA AAT GCC      209
98 Phe Glu Val Glu Ser Leu Gln Val Thr Pro Asn Asp His Ala Asn Ala
99          30          35          40
101 AGA GCA TTT TCG CAC CTG GCT ACC AAA TTG ATC GAG CAG GAG ACT GAC      257
102 Arg Ala Phe Ser His Leu Ala Thr Lys Leu Ile Glu Gln Glu Thr Asp
103          45          50          55
105 AAA GAC ACA CTC ATC TTG GAT ATC GGC AGT GCG CCT TCC AGG AGA ATG      305
106 Lys Asp Thr Leu Ile Leu Asp Ile Gly Ser Ala Pro Ser Arg Arg Met
107          60          65          70
109 ATG TCT ACG CAC AAA TAC CAC TGC GTA TGC CCT ATG CGC AGC GCA GAA      353
110 Met Ser Thr His Lys Tyr His Cys Val Cys Pro Met Arg Ser Ala Glu
111          75          80          85
113 GAC CCC GAA AGG CTC GAT AGC TAC GCA AAG AAA CTG GCA GCG GCC TCC      401
114 Asp Pro Glu Arg Leu Asp Ser Tyr Ala Lys Lys Leu Ala Ala Ala Ser
115 90          95          100          105
117 GGG AAG GTG CTG GAT AGA GAG ATC GCA GGA AAA ATC ACC GAC CTG CAG      449
118 Gly Lys Val Leu Asp Arg Glu Ile Ala Gly Lys Ile Thr Asp Leu Gln
119          110          115          120
121 ACC GTC ATG GCT ACG CCA GAC GCT GAA TCT CCT ACC TTT TGC CTG CAT      497
122 Thr Val Met Ala Thr Pro Asp Ala Glu Ser Pro Thr Phe Cys Leu His
123          125          130          135
125 ACA GAC GTC ACG TGT CGT ACG GCA GCC GAA GTG GCC GTA TAC CAG GAC      545
126 Thr Asp Val Thr Cys Arg Thr Ala Ala Glu Val Ala Val Tyr Gln Asp
127          140          145          150

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129	GTG	TAT	GCT	GTA	CAT	GCA	CCA	ACA	TCG	CTG	TAC	CAT	CAG	GCG	ATG	AAA	593
130	Val	Tyr	Ala	Val	His	Ala	Pro	Thr	Ser	Leu	Tyr	His	Gln	Ala	Met	Lys	
131		155					160					165					
133	GGT	GTC	AGA	ACG	GCG	TAT	TGG	ATT	GGG	TTT	GAC	ACC	ACC	CCG	TTT	ATG	641
134	Gly	Val	Arg	Thr	Ala	Tyr	Trp	Ile	Gly	Phe	Asp	Thr	Thr	Pro	Phe	Met	
135	170					175					180					185	
137	TTT	GAC	GCG	CTA	GCA	GGC	GCG	TAT	CCA	ACC	TAC	GCC	ACA	AAC	TGG	GCC	689
138	Phe	Asp	Ala	Leu	Ala	Gly	Ala	Tyr	Pro	Thr	Tyr	Ala	Thr	Asn	Trp	Ala	
139					190					195					200		
141	GAC	GAG	CAG	GTG	TTA	CAG	GCC	AGG	AAC	ATA	GGA	CTG	TGT	GCA	GCA	TCC	737
142	Asp	Glu	Gln	Val	Leu	Gln	Ala	Arg	Asn	Ile	Gly	Leu	Cys	Ala	Ala	Ser	
143			205					210					215				
145	TTG	ACT	GAG	GGA	AGA	CTC	GGC	AAA	CTG	TCC	ATT	CTC	CGC	AAG	AAG	CAA	785
146	Leu	Thr	Glu	Gly	Arg	Leu	Gly	Lys	Leu	Ser	Ile	Leu	Arg	Lys	Lys	Gln	
147			220					225					230				
149	TTG	AAA	CCT	TGC	GAC	ACA	GTC	ATG	TTC	TCG	GTA	GGA	TCT	ACA	TTG	TAC	833
150	Leu	Lys	Pro	Cys	Asp	Thr	Val	Met	Phe	Ser	Val	Gly	Ser	Thr	Leu	Tyr	
151		235					240					245					
153	ACT	GAG	AGC	AGA	AAG	CTA	CTG	AGG	AGC	TGG	CAC	TTA	CCC	TCC	GTA	TTC	881
154	Thr	Glu	Ser	Arg	Lys	Leu	Leu	Arg	Ser	Trp	His	Leu	Pro	Ser	Val	Phe	
155	250					255				260					265		
157	CAC	CTG	AAA	GGT	AAA	CAA	TCC	TTT	ACC	TGT	AGG	TGC	GAT	ACC	ATC	GTA	929
158	His	Leu	Lys	Gly	Lys	Gln	Ser	Phe	Thr	Cys	Arg	Cys	Asp	Thr	Ile	Val	
159			270					275					280				
161	TCA	TGT	GAA	GGG	TAC	GTA	GTT	AAG	AAA	ATC	ACT	ATG	TGC	CCC	GGC	CTG	977
162	Ser	Cys	Glu	Gly	Tyr	Val	Val	Lys	Lys	Ile	Thr	Met	Cys	Pro	Gly	Leu	
163			285					290					295				
165	TAC	GGT	AAA	ACG	GTA	GGG	TAC	GCC	GTG	ACG	TAT	CAC	GCG	GAG	GGA	TTC	1025
166	Tyr	Gly	Lys	Thr	Val	Gly	Tyr	Ala	Val	Thr	Tyr	His	Ala	Glu	Gly	Phe	
167			300					305					310				
169	CTA	GTG	TGC	AAG	ACC	ACA	GAC	ACT	GTC	AAA	GGA	GAA	AGA	GTC	TCA	TTC	1073
170	Leu	Val	Cys	Lys	Thr	Thr	Asp	Thr	Val	Lys	Gly	Glu	Arg	Val	Ser	Phe	
171		315					320					325					
173	CCT	GTA	TGC	ACC	TAC	GTC	CCC	TCA	ACC	ATC	TGT	GAT	CAA	ATG	ACT	GGC	1121
174	Pro	Val	Cys	Thr	Tyr	Val	Pro	Ser	Thr	Ile	Cys	Asp	Gln	Met	Thr	Gly	
175	330					335				340					345		
177	ATA	CTA	GCG	ACC	GAC	GTC	ACA	CCG	GAG	GAC	GCA	CAG	AAG	TTG	TTA	GTG	1169
178	Ile	Leu	Ala	Thr	Asp	Val	Thr	Pro	Glu	Asp	Ala	Gln	Lys	Leu	Leu	Val	
179			350					355					360				
181	GGA	TTG	AAT	CAG	AGG	ATA	GTT	GTG	AAC	GGA	AGA	ACA	CAG	CGA	AAC	ACT	1217
182	Gly	Leu	Asn	Gln	Arg	Ile	Val	Val	Asn	Gly	Arg	Thr	Gln	Arg	Asn	Thr	
183			365					370					375				
185	AAC	ACG	ATG	AAG	AAC	TAT	CTG	CTT	CCG	ATT	GTG	GCC	GTC	GCA	TTT	AGC	1265
186	Asn	Thr	Met	Lys	Asn	Tyr	Leu	Leu	Pro	Ile	Val	Ala	Val	Ala	Phe	Ser	
187			380					385					390				
189	AAG	TGG	GCG	AGG	GAA	TAC	AAG	GCA	GAC	CTT	GAT	GAT	GAA	AAA	CCT	CTG	1313
190	Lys	Trp	Ala	Arg	Glu	Tyr	Lys	Ala	Asp	Leu	Asp	Asp	Glu	Lys	Pro	Leu	
191		395					400					405					
193	GGT	GTC	CGA	GAG	AGG	TCA	CTT	ACT	TGC	TGC	TGC	TTG	TGG	GCA	TTT	AAA	1361

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194	Gly	Val	Arg	Glu	Arg	Ser	Leu	Thr	Cys	Cys	Cys	Leu	Trp	Ala	Phe	Lys	
195	410					415					420					425	
197	ACG	AGG	AAG	ATG	CAC	ACC	ATG	TAC	AAG	AAA	CCA	GAC	ACC	CAG	ACA	ATA	1409
198	Thr	Arg	Lys	Met	His	Thr	Met	Tyr	Lys	Lys	Pro	Asp	Thr	Gln	Thr	Ile	
199					430					435					440		
201	GTG	AAG	GTG	CCT	TCA	GAG	TTT	AAC	TCG	TTC	GTC	ATC	CCG	AGC	CTA	TGG	1457
202	Val	Lys	Val	Pro	Ser	Glu	Phe	Asn	Ser	Phe	Val	Ile	Pro	Ser	Leu	Trp	
203				445					450					455			
205	TCT	ACA	GGC	CTC	GCA	ATC	CCA	GTC	AGA	TCA	CGC	ATT	AAG	ATG	CTT	TTG	1505
206	Ser	Thr	Gly	Leu	Ala	Ile	Pro	Val	Arg	Ser	Arg	Ile	Lys	Met	Leu	Leu	
207			460					465					470				
209	GCC	AAG	AAG	ACC	AAG	CGA	GAG	TTA	ATA	CCT	GTT	CTC	GAC	GCG	TCG	TCA	1553
210	Ala	Lys	Lys	Thr	Lys	Arg	Glu	Leu	Ile	Pro	Val	Leu	Asp	Ala	Ser	Ser	
211		475				480						485					
213	GCC	AGG	GAT	GCT	GAA	CAA	GAG	GAG	AAG	GAG	AGG	TTG	GAG	GCC	GAG	CTG	1601
214	Ala	Arg	Asp	Ala	Glu	Gln	Glu	Glu	Lys	Glu	Arg	Leu	Glu	Ala	Glu	Leu	
215	490					495					500				505		
217	ACT	AGA	GAA	GCC	TTA	CCA	CCC	CTC	GTC	CCC	ATC	GCG	CCG	GCG	GAG	ACG	1649
218	Thr	Arg	Glu	Ala	Leu	Pro	Pro	Leu	Val	Pro	Ile	Ala	Pro	Ala	Glu	Thr	
219				510						515				520			
221	GGA	GTC	GTC	GAC	GTC	GAC	GTT	GAA	GAA	CTA	GAG	TAT	CAC	GCA	GGT	GCA	1697
222	Gly	Val	Val	Asp	Val	Asp	Val	Glu	Glu	Leu	Glu	Tyr	His	Ala	Gly	Ala	
223			525					530					535				
225	GGG	GTC	GTG	GAA	ACA	CCT	CGC	AGC	GCG	TTG	AAA	GTC	ACC	GCA	CAG	CCG	1745
226	Gly	Val	Val	Glu	Thr	Pro	Arg	Ser	Ala	Leu	Lys	Val	Thr	Ala	Gln	Pro	
227			540					545				550					
229	AAC	GAC	GTA	CTA	CTA	GGA	AAT	TAC	GTA	GTT	CTG	TCC	CCG	CAG	ACC	GTG	1793
230	Asn	Asp	Val	Leu	Leu	Gly	Asn	Tyr	Val	Val	Leu	Ser	Pro	Gln	Thr	Val	
231		555				560					565						
233	CTC	AAG	AGC	TCC	AAG	TTG	GCC	CCC	GTG	CAC	CCT	CTA	GCA	GAG	CAG	GTG	1841
234	Leu	Lys	Ser	Ser	Lys	Leu	Ala	Pro	Val	His	Pro	Leu	Ala	Glu	Gln	Val	
235	570				575					580				585			
237	AAA	ATA	ATA	ACA	CAT	AAC	GGG	AGG	GCC	GGC	GGT	TAC	CAG	GTC	GAC	GGA	1889
238	Lys	Ile	Ile	Thr	His	Asn	Gly	Arg	Ala	Gly	Gly	Tyr	Gln	Val	Asp	Gly	
239			590					595				600					
241	TAT	GAC	GGC	AGG	GTC	CTA	CTA	CCA	TGT	GGA	TCG	GCC	ATT	CCG	GTC	CCT	1937
242	Tyr	Asp	Gly	Arg	Val	Leu	Leu	Pro	Cys	Gly	Ser	Ala	Ile	Pro	Val	Pro	
243			605					610				615					
245	GAG	TTT	CAA	GCT	TTG	AGC	GAG	AGC	GCC	ACT	ATG	GTG	TAC	AAC	GAA	AGG	1985
246	Glu	Phe	Gln	Ala	Leu	Ser	Glu	Ser	Ala	Thr	Met	Val	Tyr	Asn	Glu	Arg	
247			620				625					630					
249	GAG	TTC	GTC	AAC	AGG	AAA	CTA	TAC	CAT	ATT	GCC	GTT	CAC	GGA	CCG	TCG	2033
250	Glu	Phe	Val	Asn	Arg	Lys	Leu	Tyr	His	Ile	Ala	Val	His	Gly	Pro	Ser	
251		635				640					645						
253	CTG	AAC	ACC	GAC	GAG	GAG	AAC	TAC	GAG	AAA	GTC	AGA	GCT	GAA	AGA	ACT	2081
254	Leu	Asn	Thr	Asp	Glu	Glu	Asn	Tyr	Glu	Lys	Val	Arg	Ala	Glu	Arg	Thr	
255	650				655					660				665			
257	GAC	GCC	GAG	TAC	GTG	TTC	GAC	GTA	GAT	AAA	AAA	TGC	TGC	GTC	AAG	AGA	2129
258	Asp	Ala	Glu	Tyr	Val	Phe	Asp	Val	Asp	Lys	Lys	Cys	Cys	Val	Lys	Arg	

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259		670		675		680		
261	GAG GAA GCG TCG GGT TTG GTG TTG GTG GGA GAG CTA ACC AAC CCC CCG							2177
262	Glu Glu Ala Ser Gly Leu Val Leu Val Gly Glu Leu Thr Asn Pro Pro							
263		685		690		695		
265	TTC CAT GAA TTC GCC TAC GAA GGG CTG AAG ATC AGG CCG TCG GCA CCA							2225
266	Phe His Glu Phe Ala Tyr Glu Gly Leu Lys Ile Arg Pro Ser Ala Pro							
267		700		705		710		
269	TAT AAG ACT ACA GTA GTA GGA GTC TTT GGG GTT CCG GGA TCA GGC AAG							2273
270	Tyr Lys Thr Thr Val Val Gly Val Phe Gly Val Pro Gly Ser Gly Lys							
271		715		720		725		
273	TCT GCT ATT ATT AAG AGC CTC GTG ACC AAA CAC GAT CTG GTC ACC AGC							2321
274	Ser Ala Ile Ile Lys Ser Leu Val Thr Lys His Asp Leu Val Thr Ser							
275	730	735		740		745		
277	GGC AAG AAG GAG AAC TGC CAG GAA ATA GTT AAC GAC GTG AAG AAG CAC							2369
278	Gly Lys Lys Glu Asn Cys Gln Glu Ile Val Asn Asp Val Lys Lys His							
279		750		755		760		
281	CGC GGG AAG GGG ACA AGT AGG GAA AAC AGT GAC TCC ATC CTG CTA AAC							2417
282	Arg Gly Lys Gly Thr Ser Arg Glu Asn Ser Asp Ser Ile Leu Leu Asn							
283		765		770		775		
285	GGG TGT CGT CGT GCC GTG GAC ATC CTA TAT GTG GAC GAG GCT TTC GCT							2465
286	Gly Cys Arg Arg Ala Val Asp Ile Leu Tyr Val Asp Glu Ala Phe Ala							
287		780		785		790		
289	TGC CAT TCC GGT ACT CTG CTG GCC CTA ATT GCT CTT GTT AAA CCT CGG							2513
290	Cys His Ser Gly Thr Leu Leu Ala Leu Ile Ala Leu Val Lys Pro Arg							
291		795		800		805		
293	AGC AAA GTG GTG TTA TGC GGA GAC CCC AAG CAA TGC GGA TTC TTC AAT							2561
294	Ser Lys Val Val Leu Cys Gly Asp Pro Lys Gln Cys Gly Phe Phe Asn							
295	810	815		820		825		
297	ATG ATG CAG CTT AAG GTG AAC TTC AAC CAC AAC ATC TGC ACT GAA GTA							2609
298	Met Met Gln Leu Lys Val Asn Phe Asn His Asn Ile Cys Thr Glu Val							
299		830		835		840		
301	TGT CAT AAA AGT ATA TCC AGA CGT TGC ACG CGT CCA GTC ACG GCC ATC							2657
302	Cys His Lys Ser Ile Ser Arg Arg Cys Thr Arg Pro Val Thr Ala Ile							
303		845		850		855		
305	GTG TCT ACG TTG CAC TAC GGA GGC AAG ATG CGC ACG ACC AAC CCG TGC							2705
306	Val Ser Thr Leu His Tyr Gly Gly Lys Met Arg Thr Thr Asn Pro Cys							
307		860		865		870		
309	AAC AAA CCC ATA ATC ATA GAC ACC ACA GGA CAG ACC AAG CCC AAG CCA							2753
310	Asn Lys Pro Ile Ile Ile Asp Thr Thr Gly Gln Thr Lys Pro Lys Pro							
311		875		880		885		
313	GGA GAC ATC GTG TTA ACA TGC TTC CGA GGC TGG GCA AAG CAG CTG CAG							2801
314	Gly Asp Ile Val Leu Thr Cys Phe Arg Gly Trp Ala Lys Gln Leu Gln							
315	890	895		900		905		
317	TTG GAC TAC CGT GGA CAC GAA GTC ATG ACA GCA GCA GCA TCT CAG GGC							2849
318	Leu Asp Tyr Arg Gly His Glu Val Met Thr Ala Ala Ala Ser Gln Gly							
319		910		915		920		
321	CTC ACC CGC AAA GGG GTA TAC GCC GTA AGG CAG AAG GTG AAT GAA AAT							2897
322	Leu Thr Arg Lys Gly Val Tyr Ala Val Arg Gln Lys Val Asn Glu Asn							
323		925		930		935		

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:707 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:711 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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